FIG. 1A

```
          10                                30                                50
GAATTCGGCACGAGCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGACATCA
          70                                90                               110
ACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCCCCAA
         130                               150                               170
CCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGAGCAGTCACGCCTTAC
                          M   D   D   S   T   E   R   E   Q   S   R   L   T
         190                               210                               230
TTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACG
 S   C   L   K   K   R   E   E   M   K   L   K   E   C   V   S   I   L   P   R
         250                               270                               290
GAAGGAAAGCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCT
 K   E   S   P   S   V   R   S   S   K   D   G   K   L   L   A   A   T   L   L
         310                               330                               350
GCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCA
 L   A   L   L   S   C   C   L   T   V   V   S   F   Y   Q   V   A   A   L   Q
         370                               390                               410
AGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGC
 G   D   L   A   S   L   R   A   E   L   Q   G   H   H   A   E   K   L   P   A
         430                               450                               470
AGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAA
 G   A   G   A   P   K   A   G   L   E   E   A   P   A   V   T   A   G   L   K
         490                               510                               530
AATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG
 I   F   E   P   P   A   P   G   E   G   N   S   S   Q   N   S   R   N   K   R
         550                               570                               590
TGCCGTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAG
 A   V   Q   G   P   E   E   T   V   T   Q   D   C   L   Q   L   I   A   D   S
```

FIG. 1B

```
      610                 630                 650
TGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAA
 E  T  P  T  I  Q  K  G  S  Y  T  F  V  P  W  L  L  S  F  K
      670                 690                 710
AAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTT
 R  G  S  A  L  E  E  K  E  N  K  I  L  V  K  E  T  G  Y  F
      730                 750                 770
TTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCA
 F  I  Y  G  Q  V  L  Y  T  D  K  T  Y  A  M  G  H  L  I  Q
      790                 810                 830
GAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTAT
 R  K  K  V  H  V  F  G  D  E  L  S  L  V  T  L  F  R  C  I
      850                 870                 890
TCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTGCAAAACT
 Q  N  M  P  E  T  L  P  N  N  S  C  Y  S  A  G  I  A  K  L
      910                 930                 950
GGAAGAAGGAGATGAACTCCAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGA
 E  E  G  D  E  L  Q  L  A  I  P  R  E  N  A  Q  I  S  L  D
      970                 990                1010
TGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGT
 G  D  V  T  F  F  G  A  L  K  L  L
     1030                1050                1070
AGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAA
     1090                1110                1130
AAAAAAAAAAAAAAAAAAAAAAAAAAGTAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA
     1150                1170
AAAAAAAAAAAAAAAAAAAAAAAACTCGGAGGGG
```

FIG. 2A

10 30 50
GAATTCGGCACGAGCTCCAAAGGCCTAGACCTTCAAAGTGCTCCTCGTGGAATGGATGAG
M D E

70 90 110
TCTGCAAAGACCCTGCCACCACCGTGCCTCTGTTTTTGCTCCGAGAAAGGAGAAGATATG
S A K T L P P P C L C F C S E K G E D M

130 150 170
AAAGTGGGATATGATCCCATCACTCCGCAGAAGGAGGAGGGTGCCTGGTTTGGGATCTGC
K V G Y D P I T P Q K E E G A W F G I C

190 210 230
AGGGATGGAAGGCTGCTGGCTGCTACCCTCCTGCTGGCCCTGTTGTCCAGCAGTTTCACA
R D G R L L A A T L L L A L L S S S F T

250 270 290
GCGATGTCCTTGTACCAGTTGGCTGCCTTGCAAGCAGACCTGATGAACCTGCGCATGGAG
A M S L Y Q L A A L Q A D L M N L R M E

310 330 350
CTGCAGAGCTACCGAGGTTCAGCAACACCAGCCGCCGCGGGTGCTCCAGAGTTGACCGCT
L Q S Y R G S A T P A A A G A P E L T A

370 390 410
GGAGTCAAACTCCTGACACCGGCAGCTCCTCGACCCCACAACTCCAGCCGCGGCCACAGG
G V K L L T P A A P R P H **N** S S R G H R

430 450 470
AACAGACGCGCTTTCCAGGGACCAGAGGAAACAGAACAAGATGTAGACCTCTCAGCTCCT
N R R A F Q G P E E T E Q D V D L S A P

490 510 530
CCTGCACCATGCCTGCCTGGATGCCGCCATTCTCAACATGATGATAATGGAATGAACCTC
P A P C L P G C R H S Q H D D N G M N L

550 570 590
AGAAACATCATTCAAGACTGTCTGCAGCTGATTGCAGACAGCGACACGCCGACTATACGA
R N I I Q D C L Q L I A D S D T P T I R

FIG. 2B

```
          610                 630                 650
AAAGGAACTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGAGGAAATGCCTTGGAG
K  G  T  Y  T  F  V  P  W  L  L  S  F  K  R  G  N  A  L  E
          670                 690                 710
GAGAAAGAGAACAAAATAGTGGTGAGGCAAACAGGCTATTTCTTCATCTACAGCCAGGTT
E  K  E  N  K  I  V  V  R  Q  T  G  Y  F  F  I  Y  S  Q  V
          730                 750                 770
CTATACACGGACCCCATCTTTGCTATGGGTCATGTCATCCAGAGGAAGAAAGTACACGTC
L  Y  T  D  P  I  F  A  M  G  H  V  I  Q  R  K  K  V  H  V
          790                 810                 830
TTTGGGGACGAGCTGAGCCTGGTGACCCTGTTCCGATGTATTCAGAATATGCCCAAAACA
F  G  D  E  L  S  L  V  T  L  F  R  C  I  Q  N  M  P  K  T
          850                 870                 890
CTGCCCAACAATTCCTGCTACTCGGCTGGCATCGCGAGGCTGGAAGAAGGAGATGAGATT
L  P  N  N  S  C  Y  S  A  G  I  A  R  L  E  E  G  D  E  I
          910                 930                 950
CAGCTTGCAATTCCTCGGGAGAATGCACAGATTTCACGCAACGGAGACGACACCTTCTTT
Q  L  A  I  P  R  E  N  A  Q  I  S  R  N  G  D  D  T  F  F
          970                 990                1010
GGTGCCCTAAAACTGCTGTAACTCACTTGCTGGAGTGCGTGATCCCCTTCCCTCGTCTTC
G  A  L  K  L  L
         1030                1050                1070
TCTGTACCTCCGAGGGAGAAACAGACGACTGGAAAAACTAAAAGATGGGGAAAGCCGTCA
         1090                1110                1130
GCGAAAGTTTTCTCGTGACCCGTTGAATCTGATCCAAACCAGGAAATATAACAGACAGCC
         1150                1170                1190
```

FIG. 3A

```
         1                                                    50
Hagp3    MDDSTER.EQ SRLTSCLKKR EEMKLKECVS ILPRKESPSV RSSKDGKLLA
Magp3    MDESAKTLPP PCLCFCSEKG EDMKVGYDPI TPQKEEGAWF GICRDGRLLA
 cons    MD.S...... ..L..C..K. E.MK...... .....E.... ....DG.LLA

         51                                                  100
Hagp3    ATLLLALLSC CLTVVSFYQV AALQGDLASL RAELQGHHAE KLPAGAGAPK
Magp3    ATLLLALLSS SFTAMSLYQL AALQADLMNL RMELQSYRGS ATPAAAGAPE
 cons    ATLLLALLS. ..T..S.YQ. AALQ.DL..L R.ELQ..... ..PA.AGAP.

        101                                                  150
Hagp3    AGLEEAPAVT AGLKIFEPPA PGEGNSSQNS RNKRAVQGPE ET........
Magp3    ........LT AGVKLLTPAA PRPHNSSRGH RNRRAFQGPE ETEQDVDLSA
 cons    .........T AG.K...P.A P...NSS... RN.RA.QGPE ET........

         151                             B                   200
Hagp3    .......... .......... ...VTQDCLQ LIADSETPTI QKGSYTFVPW
Magp3    PPAPCLPGCR HSQHDDNGMN LRNIIQDCLQ LIADSDTPTI RKGTYTFVPW
 cons    .......... .......... .....QDCLQ LIADS.TPTI .KG.YTFVPW
```

FIG. 3B

```
        B'         C'        C          D          E         250
Hagp3   LLSFKRGSAL EEKENKILVK ETGYFFIYGQ VLYTDKTYAM GHLIQRKKVH
Magp3   LLSFKRGNAL EEKENKIVVR QTGYFFIYSQ VLYTDPIFAM GHVIQRKKVH
 cons   LLSFKRG.AL EEKENKI.V. .TGYFFIY.Q VLYTD...AM GH.IQRKKVH

        251   F                         G          H        300
Hagp3   VFGDELSLVT LFRCIQNMPE TLPNNSCYSA GIAKLEEGDE LQLAIPRENA
Magp3   VFGDELSLVT LFRCIQNMPK TLPNNSCYSA GIARLEEGDE IQLAIPRENA
 cons   VFGDELSLVT LFRCIQNMP. TLPNNSCYSA GIA.LEEGDE .QLAIPRENA

        301        I    317
Hagp3   QISLDGDVTF FGALKLL
Magp3   QISRNGDDTF FGALKLL
 cons   QIS..GD.TF FGALKLL
```

FIG. 4A

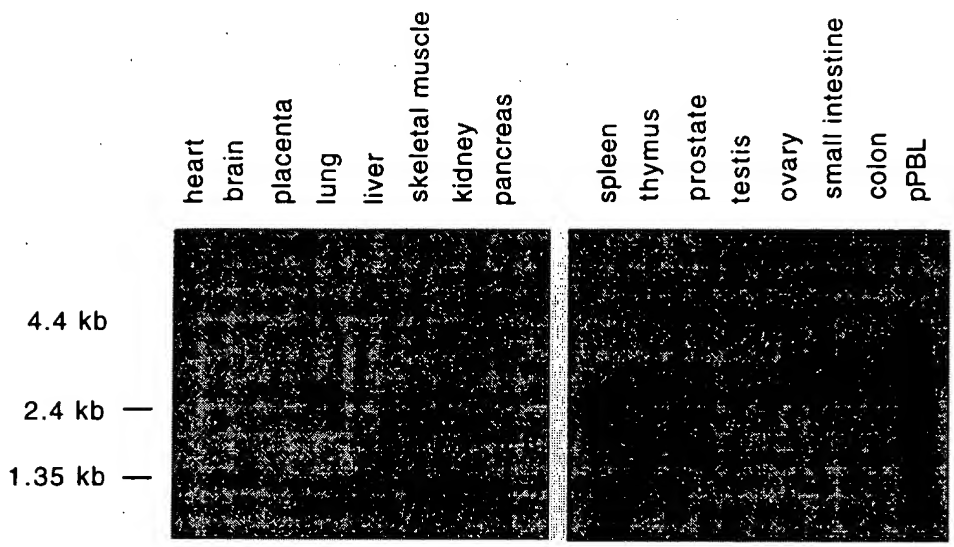

heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
spleen
thymus
prostate
testis
ovary
small intestine
colon
pPBL
4.4 kb
2.4 kb
1.35 kb

FIG. 4B

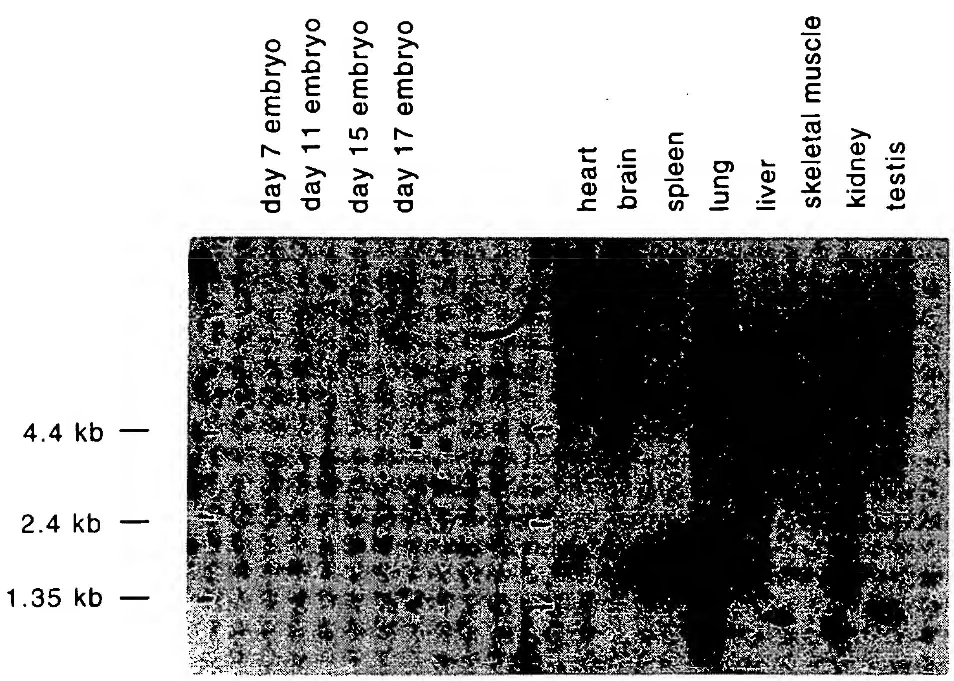

day 7 embryo
day 11 embryo
day 15 embryo
day 17 embryo
heart
brain
spleen
lung
liver
skeletal muscle
kidney
testis
4.4 kb
2.4 kb
1.35 kb

FIG. 5A

FIG. 5B

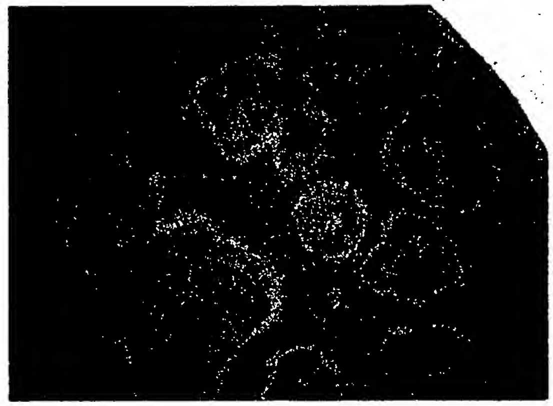


FIG. 5C

FIG. 5D

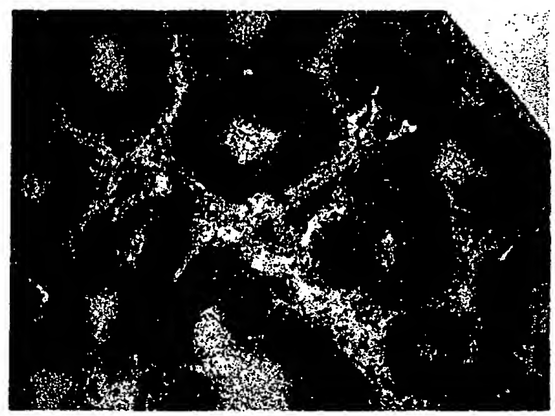


FIG. 5E

E

FIG. 5F

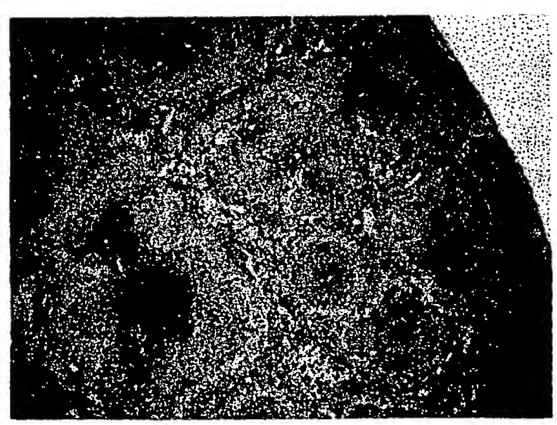


FIG. 6A

FIG. 6B

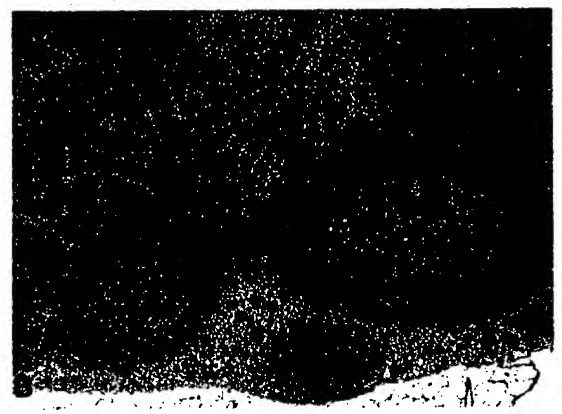


FIG. 6C

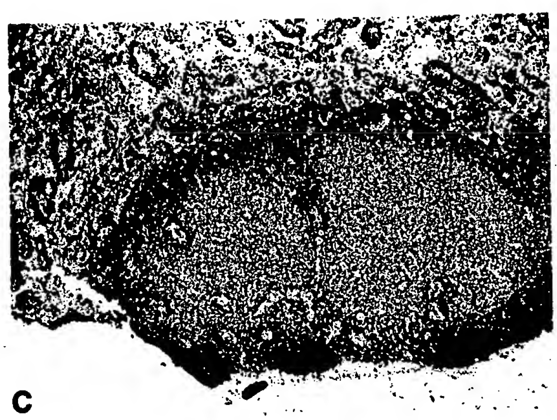


FIG. 6D

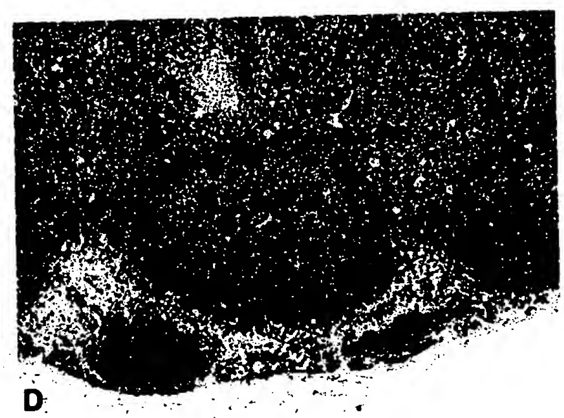


FIG. 6E

FIG. 6F

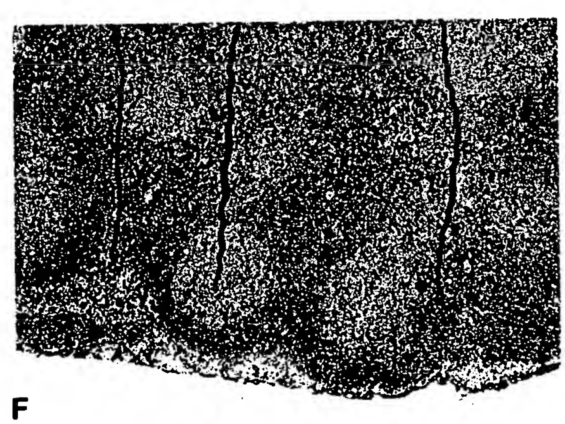


FIG. 7A

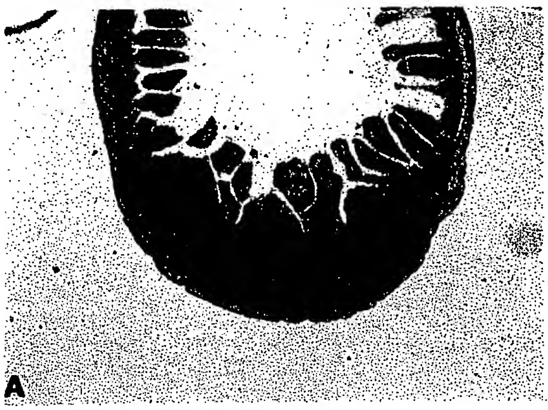


FIG. 7B

FIG. 7C

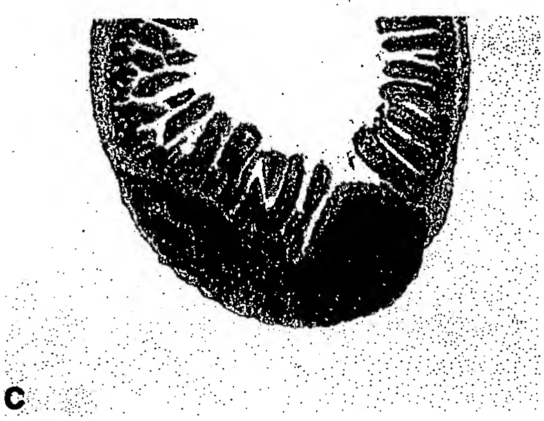


FIG. 7D

FIG. 7E

FIG. 7F

FIG. 8A

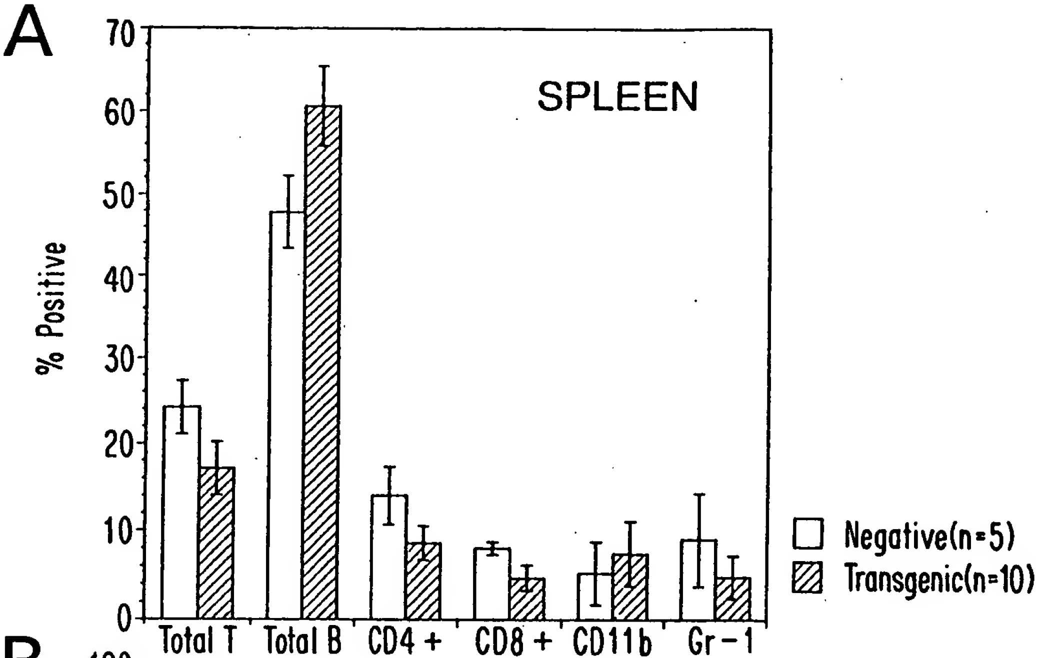


FIG. 8B

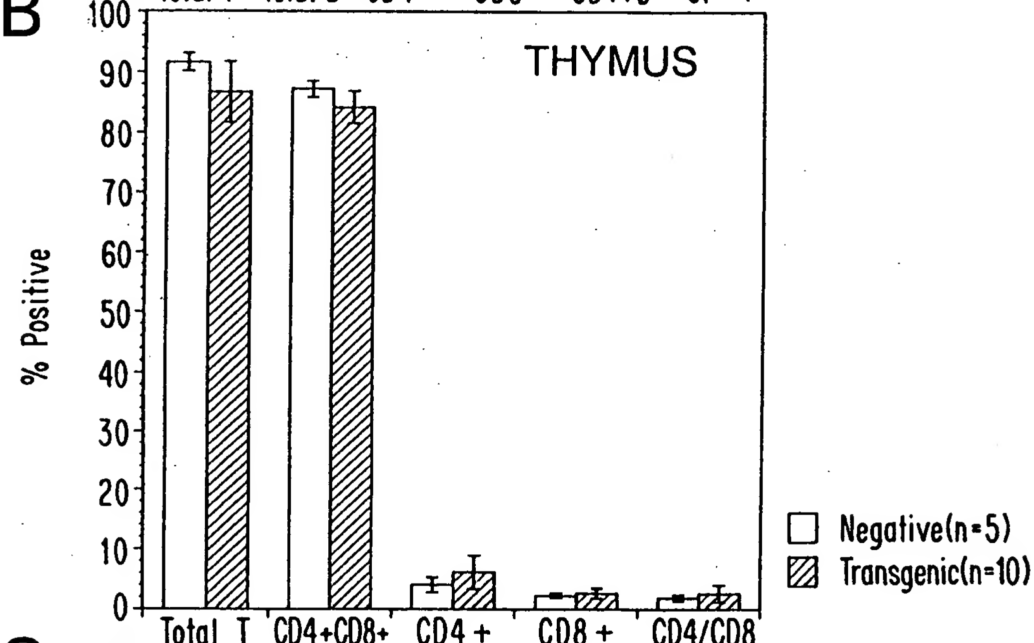


FIG. 8C

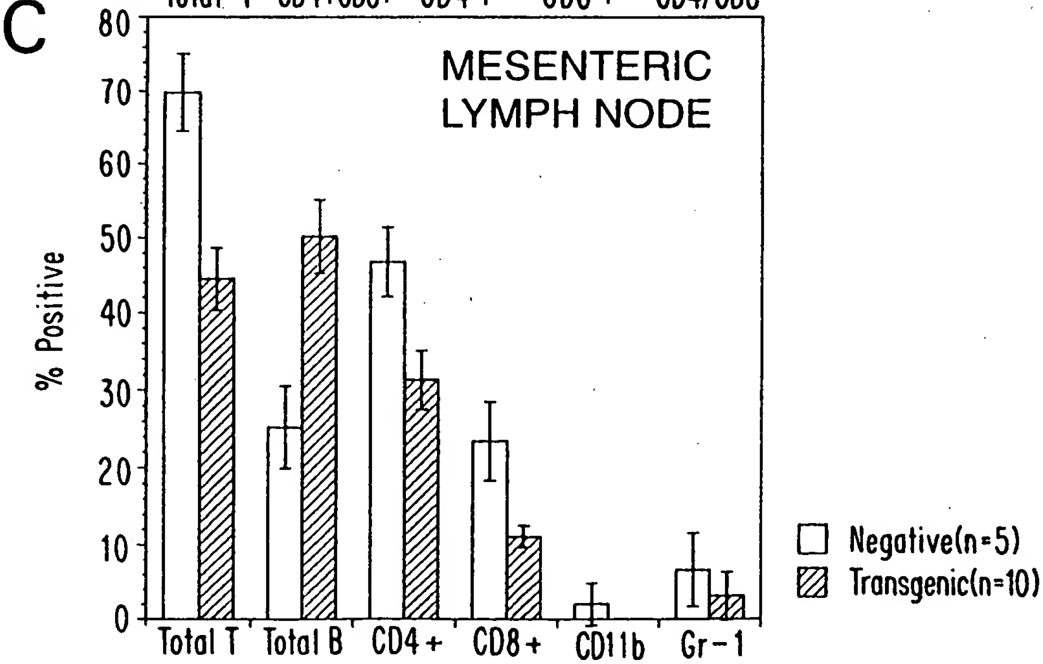


FIG. 9A

```
             B                  B/B' loop                 B'     C'      C          D        D/E loop   E
      -----+PAAHLT--P--------------------L-W--------A-LS-GV-L-N----LVV---GLYFIYSQV-F+GQ-CP-------V-L             Consensus
139-  EKKELRKVAHLTGKSN---------------SRS-MPLEWEDTYGI--VLLS-GVKYKK--GGLVINETGLYFVYSKVYFRGQSCN------NLPL           Human FasL
137-  EKKEPRSVAHLTGNPH---------------SRS-IPLEWEDTYGT--ALIS-GVKYKK--GGLVINETGLYFVYSKVYFRGQSCN------NQPL           Mouse FasL
136-  ETKKPRSVAHLTGNPR---------------SRS-IPLEWEDTYGT--ALIS-GVKYKK--GGLVINEAGLYFVYSKVYFRGQSCN------SQPL           Rat FasL
116-  GDQNPQIAAHVISEASS--------------KTT-SVLQWAEKGYY--TMSNNLVTLENG-KQLTVKRQGLYYIYAQVTFCSNREA----SSQAPF          Human CD40L
115-  GDEDPQIAAHVVSEANS--------------NAA-SVLQWAKKGYY--TMKSNLVMLENG-KQLTVKREGLYYVYTQVTFCSNREP----SSQRPF          Mouse CD40L
142-  ---VTQDCLQLIADSETPTIQ--------KGSY--TFVPWLLSFKR-GSALE---EKEN--KIL-VKETGYFFIYGQVLYT-DKT-----YAMGHL          Human AGP3
163-  LRNIIQDCLQLIADSDTPTIR--------KGTY--TFVPWLLSFKR-GNALE---EKEN--KI-VVRQTGYFFIYSQVLYT-DPI-----FAMGHV          Mouse AGP3
157-  GKPEAQPFAHLTINAASIP----------SGSHKVTLSSWYHDRGW--AKISN-MTLSNG-K-LRVNQDGFYYLYANICFRHHETS----GSVPTD          Mouse OPGL
158-  SKLEAQPFAHLTINATDIP----------SGSHKVSLSSWYHDRGW--AKISN-MTFSNG-K-LIVNQDGFYYLYANICFRHHETS----GDLATE          Human OPGL
116-  ERGPQRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH-SFLSN-LHLRNG-E-LVIHEKGFYYIYSQTYFRFQEE------IKENT           Human TRAIL
120-  GGRPQKVAAHITGITRRSNSALIPISKDGKTLGQKIESWESSRKGH-SFLNH-VLFRNG-E-LVIEQEGLYYIYSQTYFRFQEAEDASKMVSKD-          Mouse TRAIL
92-   RAPFKKSWAYLQVAKH---------------LNK-TKLSWNKDG-----ILH-GVRYQD--GNLVIQFPGLYFIICQLQFLVQ-CP----NNSVDL         Human CD30L
97-   STPSKKSWAYLQVSKH---------------LNN-TKLSWNEDG-----TIH-GLIYQD--GNLIVQFPGLYFIVCQLQFLVQ-CS----NHSVDL         Mouse CD30L
82-   DLSPGLPAAHLIGAP----------------LKGQ-GLGWETTKEQ--AFLTSGTQFSDA-EGLALPQDGLYYLYCLVGYRGRAPPGGGDPQGRSV         Human LyTβ
148-  DLNPELPAAHLIGAW----------------MSGQ-GLSWEASQEE--AFLRSGAQFSPT-HGLALPQDGVYYLYCHVGYRGRTPPA-GRSRARSL         Mouse LyTβ
57-   AHSTLKPAAHLIGDP----------------SKQNS-LLWRANTDR--AFLQDGFSLSN--NSLLVPTSGIYFVYSQVVFSGKAYSPKATSSPLYL         Human TNFβ
54-   THGILKPAAHLVGYP----------------SKQNS-LLWRASTDR--AFLRHGFSLSN--NSLLIPTSGLYFVYSQVVFSGESCSPRAIPTPIYL         Mouse TNFβ
82-   RTPSDKPVAHVVANP----------------QAEGQ-LQWLNRRAN--ALLANGVELRD--NQLVVPSEGLYLIYSQVLFKGQGCP----STHVLL          Human TNFα
85-   QNSSDKPVAHVVANH----------------QVEEQ-LEWLSQRAN--ALLANGMDLKD--NQLVVPADGLYLVYSQVLFKGQGCP-----DYVLL          Mouse TNFα
```

FIG. 9B

```
        E        E/F loop       F          F/G loop              G               H      H/I loop       I
     -H-V---V--------YP----LLS---T--C-------------W--S-YLGGVF-L--GD-LYVNV---S---F-----TFFGLFKL                 Consensus
08-  SHKVYMRNS------KYPQDLVMMEGKMMSYC--------TTGQMWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQ-TFFGLYKL          -281   Human FasL
06-  NHKVYMRNS------KYPEDLVLMEEKRLNYC--------TTGQIWAHSSYLGAVFNLTSADHLYVNISQLSLINFEESK-TFFGLYKL          -279   Mouse FasL
05-  SHKVYMRNF------KYPGDLVLMEEKKLNYC--------TTGQIWAHSSYLGAVFNLTVADHLYVNISQLSLINFEESK-TFFGLYKL          -278   Rat FasL
90-  IASLCLKS-------PGRFERILLRAANTHSSAKPC---------GQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGF-TSFGLLKL          -261   Human CD40L
89-  IVGLWLKP-------SIGSERILLKAANTHSSSQLC---------EQQSVHLGGVFELQAGASVFVNVTEASQVIHRVGF-SSFGLLKL          -260   Mouse CD40L
12-  IQRKKVHV--------FGDELSLVTLFRCIQNMPETL-------P-NNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL         -285   Human AGP3
36-  IQRKKVHV--------FGDELSLVTLFRCIQNMPKTL-------P-NNSCYSAGIARLEEGDEIQLAIPRENAQISRNGDDTFFGALKLL         -309   Mouse AGP3
34-  YLQLMVYVVKTSI--KIPSSHNLMKGGSTKNWSGN-----SE--FHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDA-TYFGAFKVQDID     -316   Mouse OPGL
35-  YLQLMVYVTKTSI--KIPSSHTLMKGGSTKYWSGN-----SE--FHFYSINVGGFFKLRSGEEISIEVSNPSLLDPDQDA-TYFGAFKVRDID     -317   Human OPGL
01-  K-NDKQMVQYIYKYTSYPDPILLMKSARNSCWSKD-----AE--YGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA-SFFGAFLVG         -281   Human TRAIL
10-  KVRTKQLVQYIYKYTSYPDPIVLMKSARNSCWSRD-----AE--YGLYSIYQGGLFELKKNDRIFVSVTNEHLMDLDQEA-SFFGAFLIN         -291   Mouse TRAIL
59-  KLELLIN------------KHIKKQALVTVCESGMQTK--HVYQNLSQFLLDYLQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD         -234   Human CD30L
64-  TLQLLIN------------SKIKKQTLVTVCESGVQSK--NIYQNLSQFLLHYLQVNSTISVRVDNFQYVDTNTFPLDNVLSVFLYSSSD         -239   Mouse CD30L
58-  TLRSSLYRAGGA--YGPGTPELLLEGAETVTPVLDPARRQGYGPLWYTSVGFGGLVQLRRGERVYVNISHPDMVDFARGK-TFFGAVMVG         -244   Human LyTβ
23-  TLRSALYRAGGA--YGRGSPELLLEGAETVTPVVDPI---GYGSLWYTSVGFGGLAQLRSGERVYVNISHPDMVDYRRGK-TFFGAVMVG         -306   Mouse LyTβ
32-  AHEVQLFSS------QYPFHVPLLSSQKMVYP--------GLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPHLVLSPST-VFFGAFAL          -205   Human TNFβ
29-  AHEVQLFSS------QYPFHVPLLSAQKSVYP--------GLQGPWVRSMYQGAVFLLSKGDQLSTHTDGISHLHFSPSS-VFFGAFAL          -202   Mouse TNFβ
53-  THTISRIAV------SYQTKVNLLSAIKSPCQRETPEG--AEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL         -233   Human TNFα
55-  THTVSRFAI------SYQEKVNLLSAVKSPCPKDTPEG--AELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL         -235   Mouse TNFα
```

FIG. 10A

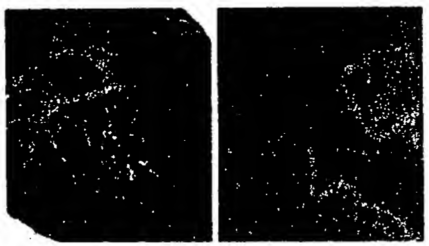


FIG. 10D

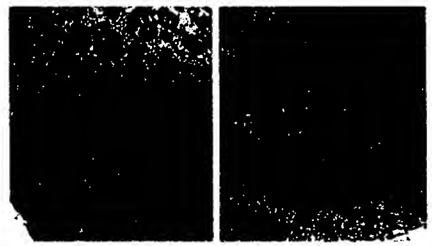


FIG. 10G

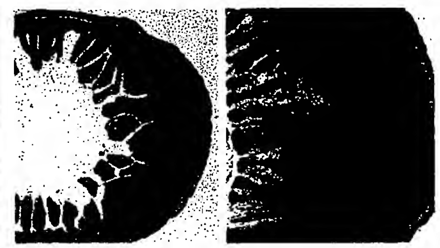


FIG. 10B

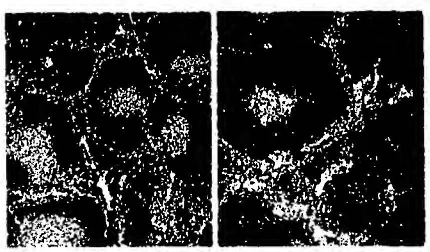


FIG. 10E

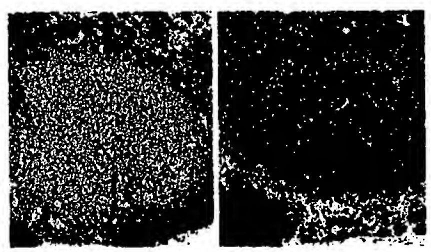


FIG. 10H

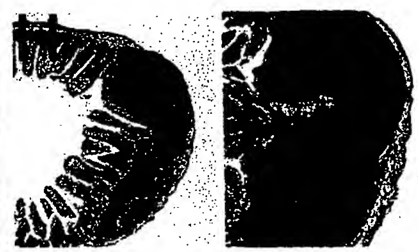


FIG. 10C

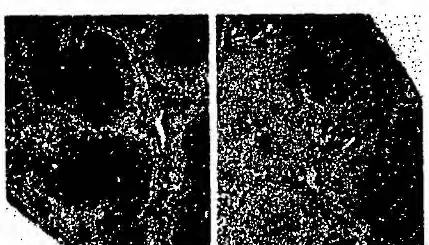


FIG. 10F

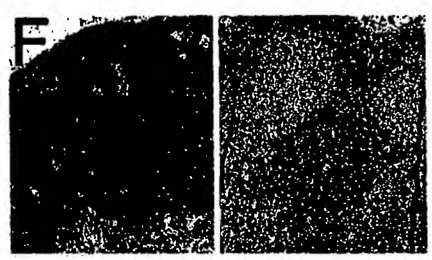


FIG. 10I

FIG. 11A

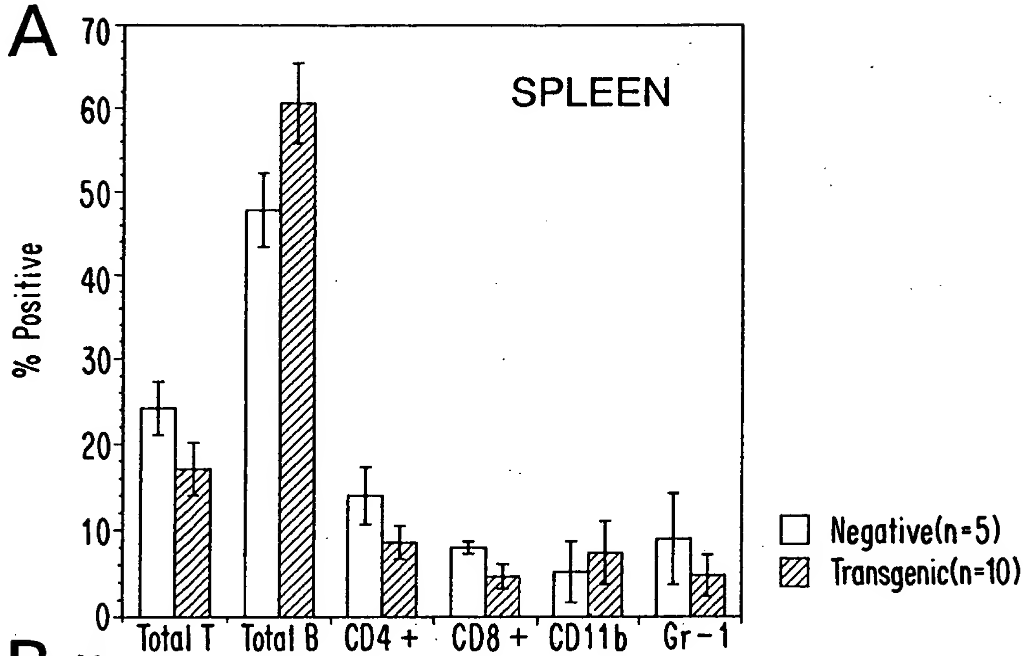


FIG. 11B

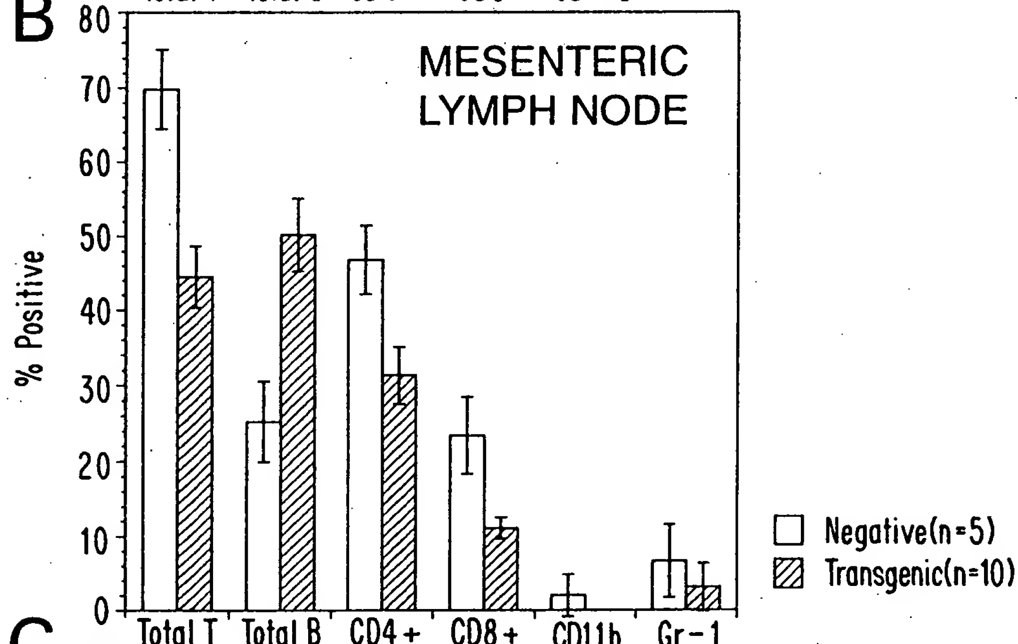


FIG. 11C

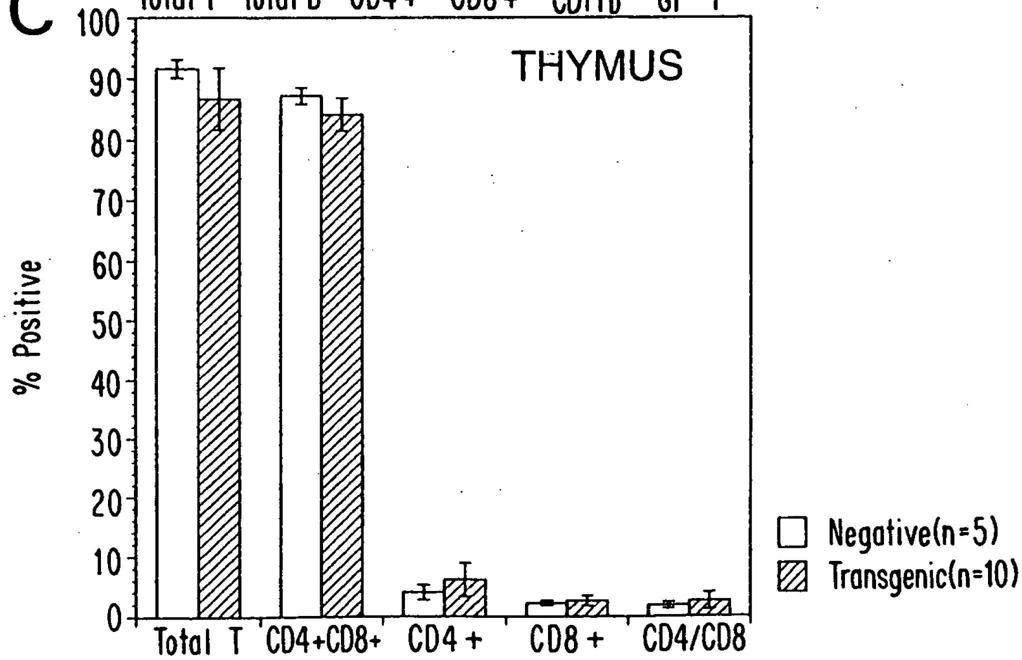


FIG. 12A

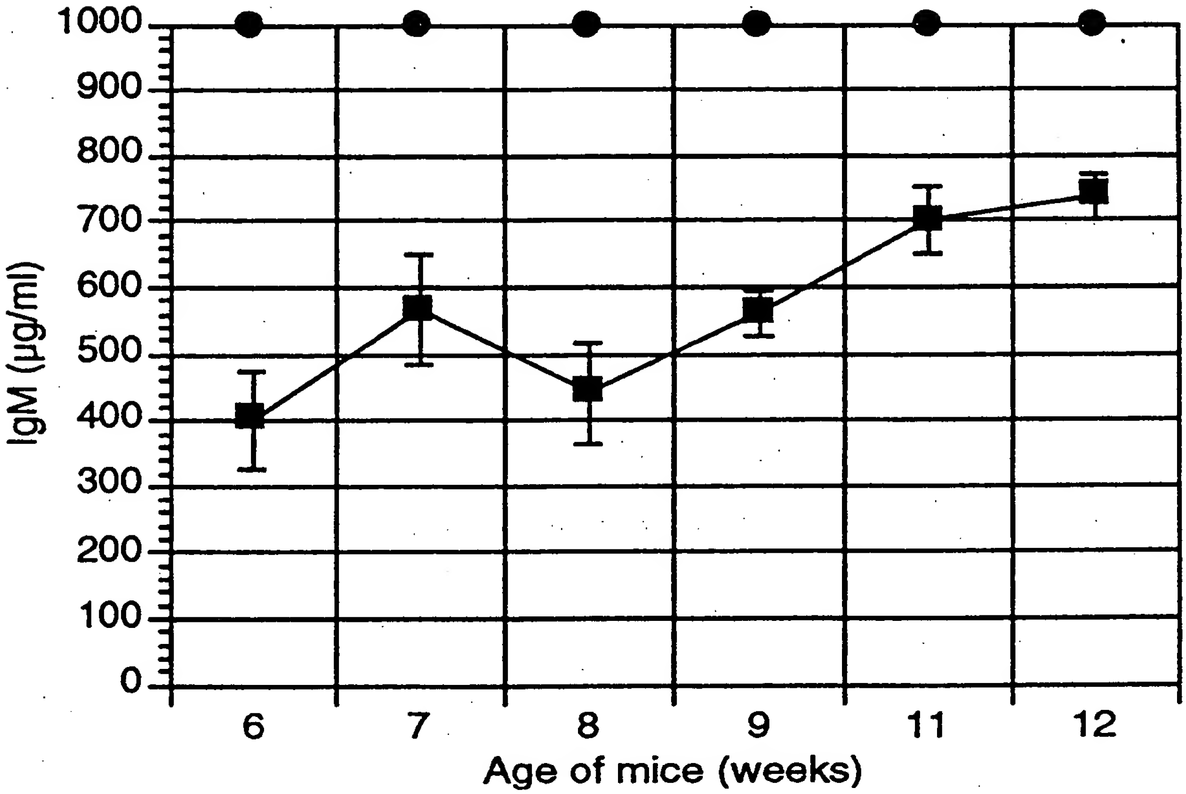


FIG. 12B

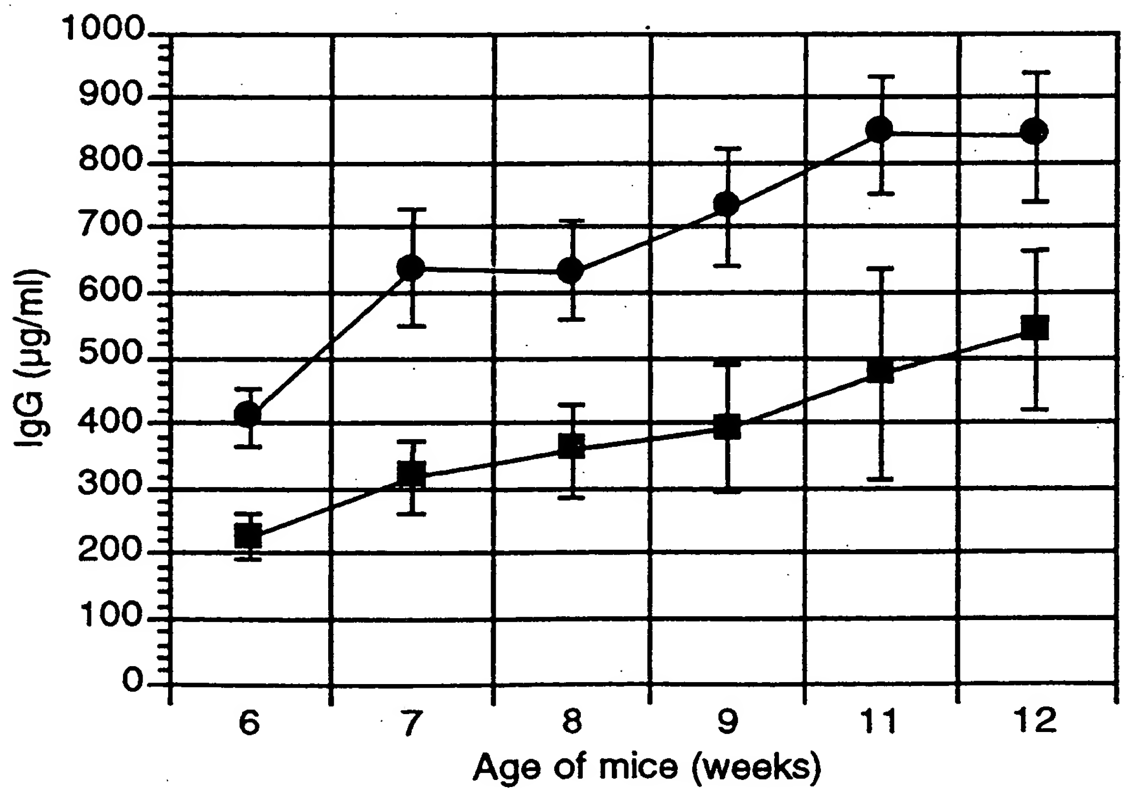


FIG. 12C

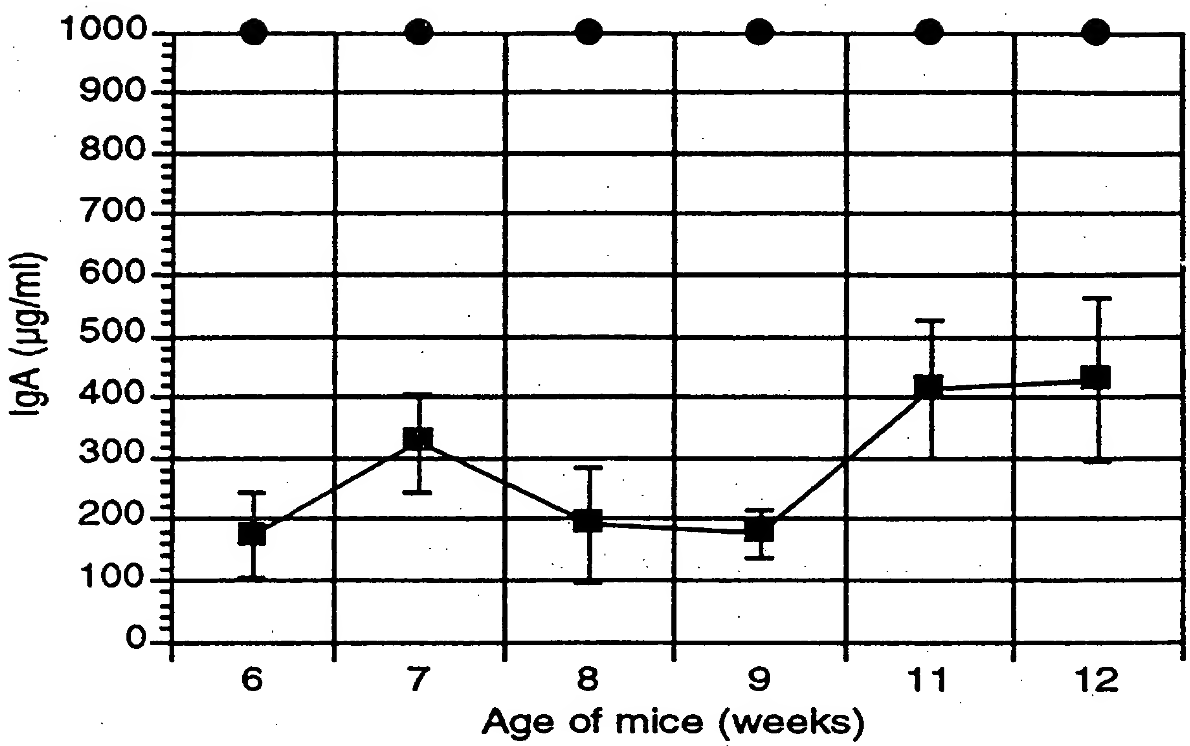


FIG. 12D

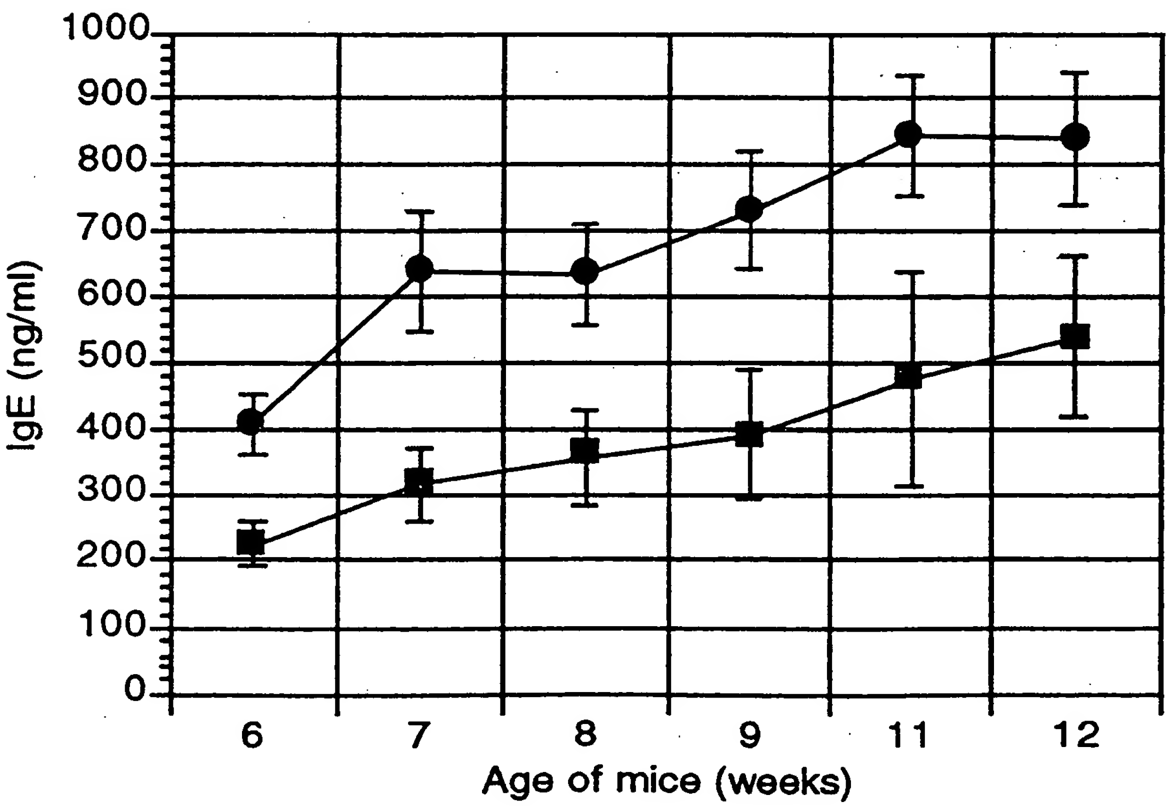


FIG. 13A

FIG. 13D

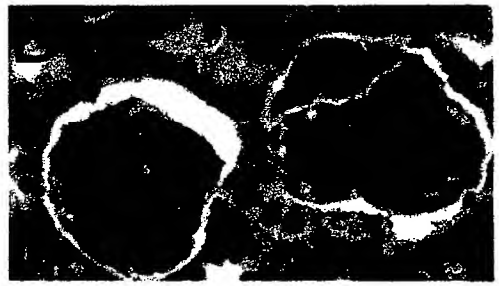


FIG. 13G

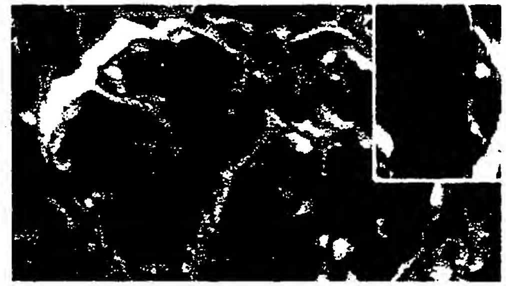


FIG. 13B

FIG. 13E

FIG. 13H

FIG. 13C

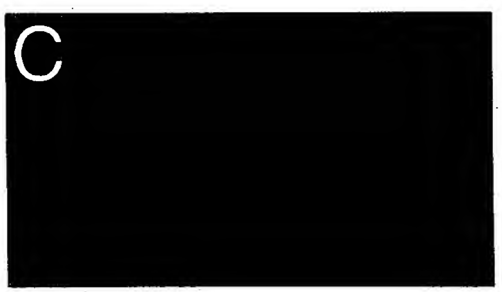


FIG. 13F

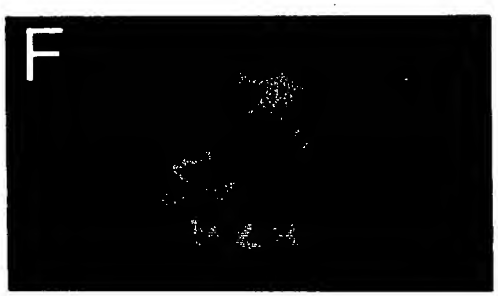


FIG. 13I

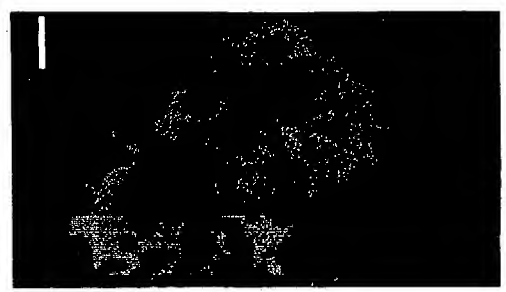


FIG. 14A

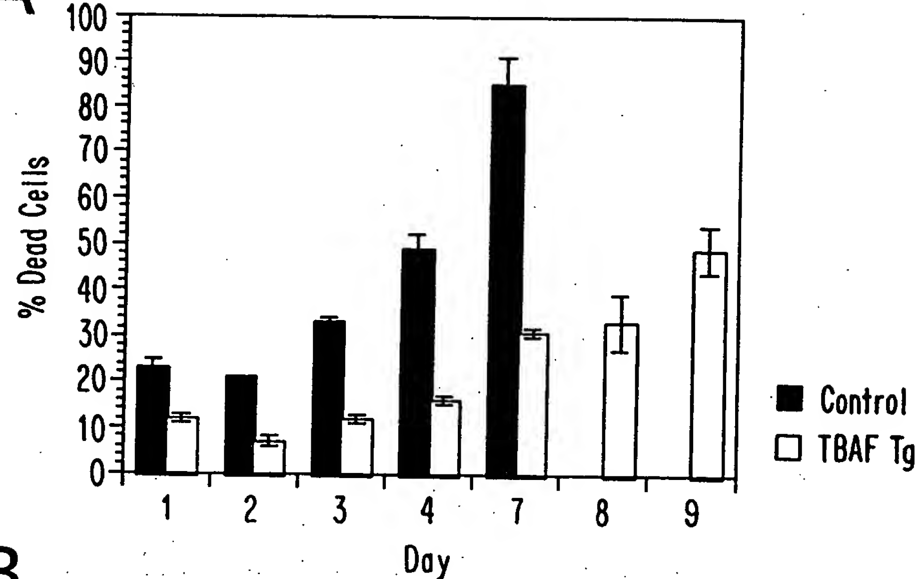


FIG. 14B

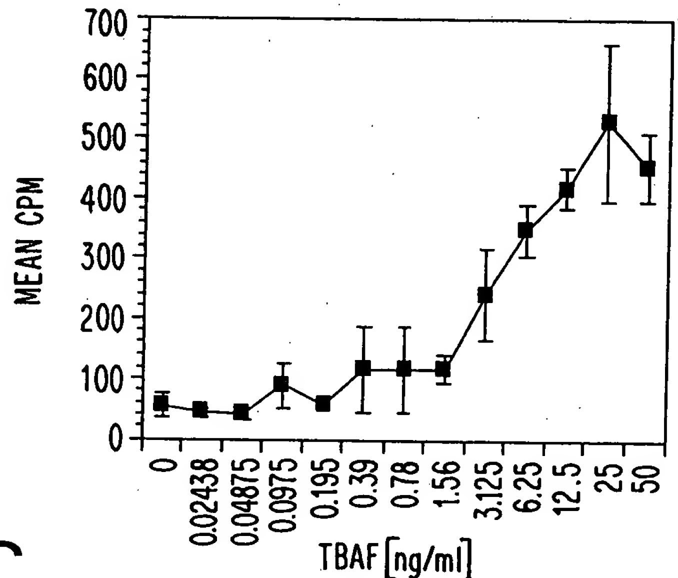


FIG. 14C

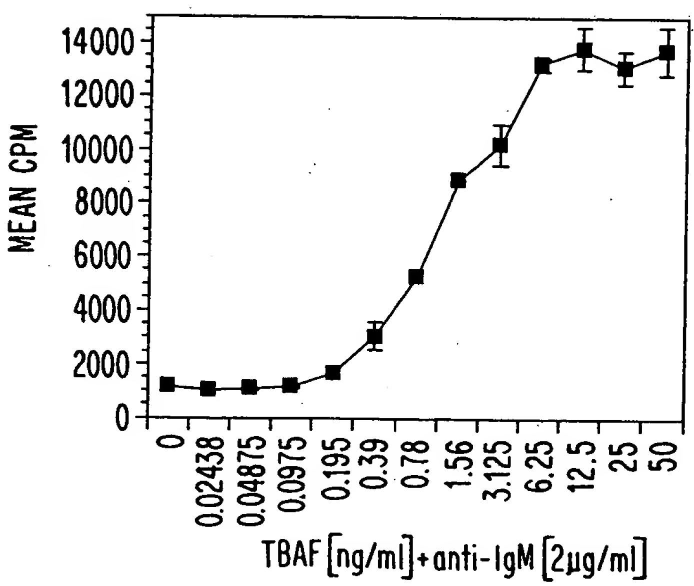
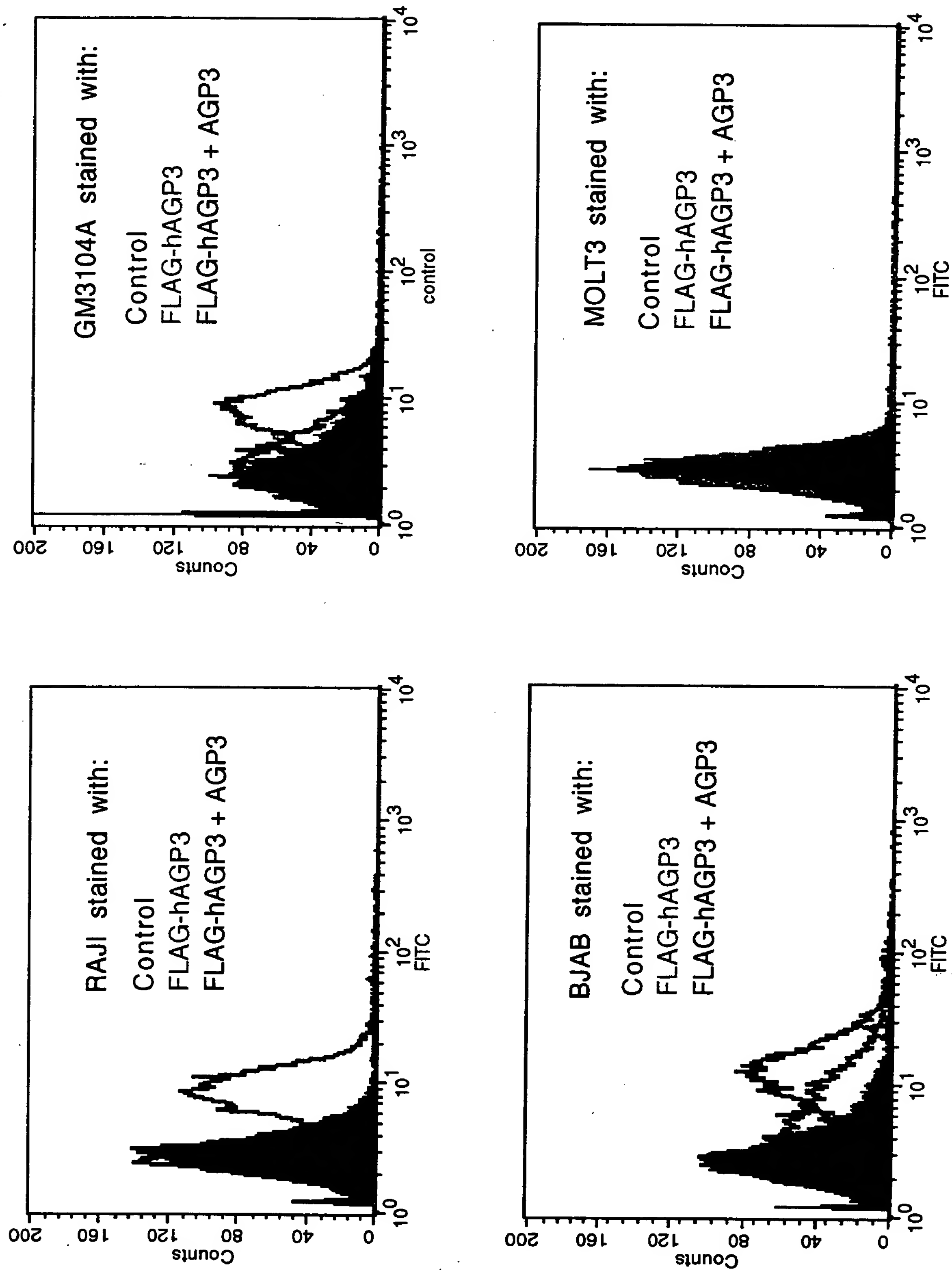


FIG. 15



GM3104A stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
control
MOLT3 stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
FITC
RAJI stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
FITC
BJAB stained with:
Control
FLAG-hAGP3
FLAG-hAGP3 + AGP3
Counts
FITC

FIG. 16

Alignment of AGP3-binding pools 13B4 and 13H11
N-terminal sequence

```
  1 GTCGACCCACGCGTCCG.......ATCCTGAGTAATGAGTGGCCTGGGCC 43
    |||||||||||||||||       ||||||||||||||||||||||||||
  1 GTCGACCCACGCGTCCGAATAAGCATCCTGAGTAATGAGTGGCCTGGGCC 50

 44 GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 93
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 100

 94 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 143
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 150

144 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTTGCAACC 193
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTTGCAACC 200

194 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 243
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 250

244 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 293
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 300

294 TGCCTCCATCTGTGGACAGCACCCTAAGCAATGTGCATACTTCTGTGAGA 343
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 TGCCTCCATCTGTGGACAGCACCCTAAGCAATGTGCATACTTCTGTGAGA 350

344 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 393
    ||||||||||||||||||||||||||||||||||||||||||||||||||
351 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 400
```

FIG. 17

Human AGP3 receptor sequence

```
GTCGACCCACGCGTCCGATCCTGAGTAATGAGTGGCCTGGGCCGGAGCAGGCGAGGTGGC
                                        M  S  G  L  G  R  S  R  R  G  G
CGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCACAGGGCCTGTGGACAGGGGTGGCTATG
R  S  R  V  D  Q  E  E  R  F  P  Q  G  L  W  T  G  V  A  M
AGATCCTGCCCCGAAGAGCAGTACTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAA
R  S  C  P  E  E  Q  Y  W  D  P  L  L  G  T  C  M  S  C  K
ACCATTTGCAACCATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGC
T  I  C  N  H  Q  S  Q  R  T  C  A  A  F  C  R  S  L  S  C
CGCAAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTGTGCCTCC
R  K  E  Q  G  K  F  Y  D  H  L  L  R  D  C  I  S  C  A  S
ATCTGTGGACAGCACCCTAAGCAATGTGCATACTTCTGTGAGAACAAGCTCAGGAGCCCA
I  C  G  Q  H  P  K  Q  C  A  Y  F  C  E  N  K  L  R  S  P
GTGAACCTTCCACCAGAGCTCAGGAGACAGCGGAGTGGAGAAGTTGAAAACAATTCAGAC
V  N  L  P  P  E  L  R  R  Q  R  S  G  E  V  E  N  N  S  D
AACTCGGGAAGGTACCAAGGACTGGAGCACAGAGGCTCAGAAGCAAGTCCAGCTCTCCCG
N  S  G  R  Y  Q  G  L  E  H  R  G  S  E  A  S  P  A  L  P
GGGCTGAAGCTGAGTGCAGATCAGGTGGCCCTGGTCTACAGCACGCTGGGGCTCTGCCTG
G  L  K  L  S  A  D  Q  V  A  L  V  Y  S  T  L  G  L  C  L
TGTGCCGTCCTCTGCTGCTTCCTGGTGGCGGTGGCCTGCTTCCTCAAGATGAGGGGGGAT
C  A  V  L  C  C  F  L  V  A  V  A  C  F  L  K  M  R  G  D
CCCTGCTCCTGCCAGCCCCGCTCAAGGCCCCGTCAAAGTCCGGCCAAGTCTTCCCAGGAT
P  C  S  C  Q  P  R  S  R  P  R  Q  S  P  A  K  S  S  Q  D
CACGCGATGGAAGCCGGCAGCCCTGTGAGCACATCCCCCGAGCCAGTGGAGACCTGCAGC
H  A  M  E  A  G  S  P  V  S  T  S  P  E  P  V  E  T  C  S
TTCTGCTTCCCTGAGTGCAGGGCGCCCACGCAGGAGAGCGCAGTCACGCCTGGGACCCCC
F  C  F  P  E  C  R  A  P  T  Q  E  S  A  V  T  P  G  T  P
GACCCCACTTGTGCTGGAAGGTGGGGGTGCCACACCAGGACCACAGTCCTGCAGCCTTGC
D  P  T  C  A  G  R  W  G  C  H  T  R  T  T  V  L  Q  P  C
CCACACATCCCAGACAGCGGCCTTGGCATTGTGTGTGTGCCTGCCCAGGAGGGGGGCCCA
P  H  I  P  D  S  G  L  G  I  V  C  V  P  A  Q  E  G  G  P
GGTGCATAAATGGGGGTCAGGGAGGGAAAGGAGGAGGGAGAGAGATGGAGAGGAGGGGAG
G  A
AGAGAAAGAGAGGTGGGGAGAGGGGAGAGAGATATGAGGAGAGAGAGACAGAGGAGGCAG
AGAGGGAGAGAAACAGAGGAGACAGAGAGGGAGAGAGAGACAGAGGGAGAGAGAGACAGA
GAGGAAGAGAGGCAGAGAGGGAAAGAGGCAGAGAAGGAAAGAGACAGGCAGAGAAGGAGA
GAGGCAGAGAGGGAGAGAGGCAGAGAGGGAGAGAGGCAGAGAGACAGAGAGGGAGAGAGG
GACAGAGAGAGATAGAGCAGGAGGTCGGGGCACTCTGAGTCCCAGTTCCCAGTGCAGCTG
TAGGTCGTCATCACCTAACCACACGTGCAATAAAGTCCTCGTGCCTGCTGCTCACAGCCC
CCGAGAGCCCCTCCTCCTGG
```

FIG. 18

AGP3 receptor protein structure

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMR

SCPEEQYWDPLLGTCMSCKTICNHQSQRTCAAFCRSL I

SCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENK II

LRSPVNLPPELRRQRSGEVENNSDNSGRYQGLEHRGSE stalk
ASPALPGLKLSADQVAVYS

<u>TLGLCLCAVLCCFLVAVACFL</u> TM

KMRGDPCSCQPRSRPRQSPAKSSQDHAMEAGSPVSTSP IC
EPVETCSFCFPECRAPTQESAVTPGTPDTCAGRWGCHT
RTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

FIG. 19

Alignment of AGP3 receptor and TNFR1 extracellular domain

```
        10        20        30        40        50         60
LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTTCMSCKTICNHQS-QR    AGP3R
                                  ||: :|  |  :: |  | | |:: :
VLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNSIC--C-TKCHKGTYLYN   TNFR1
      20        30        40        50          60        70

         70         80        90       100       110
TCAAFCRSLSCRK-EQGKF-YDHLLRDCISCASICGQHPKQCAYFCENKLRSPVNLPPE    AGP3R
              | :   :: :||: |:|:|    :: || |:|| | | ::  |
DCPGPGQDTDCRECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRDTVCGCRK   TNFR1
        80        90       100       110       120
```

FIG. 20

Human AGP3 receptor mRNA tissue distribution

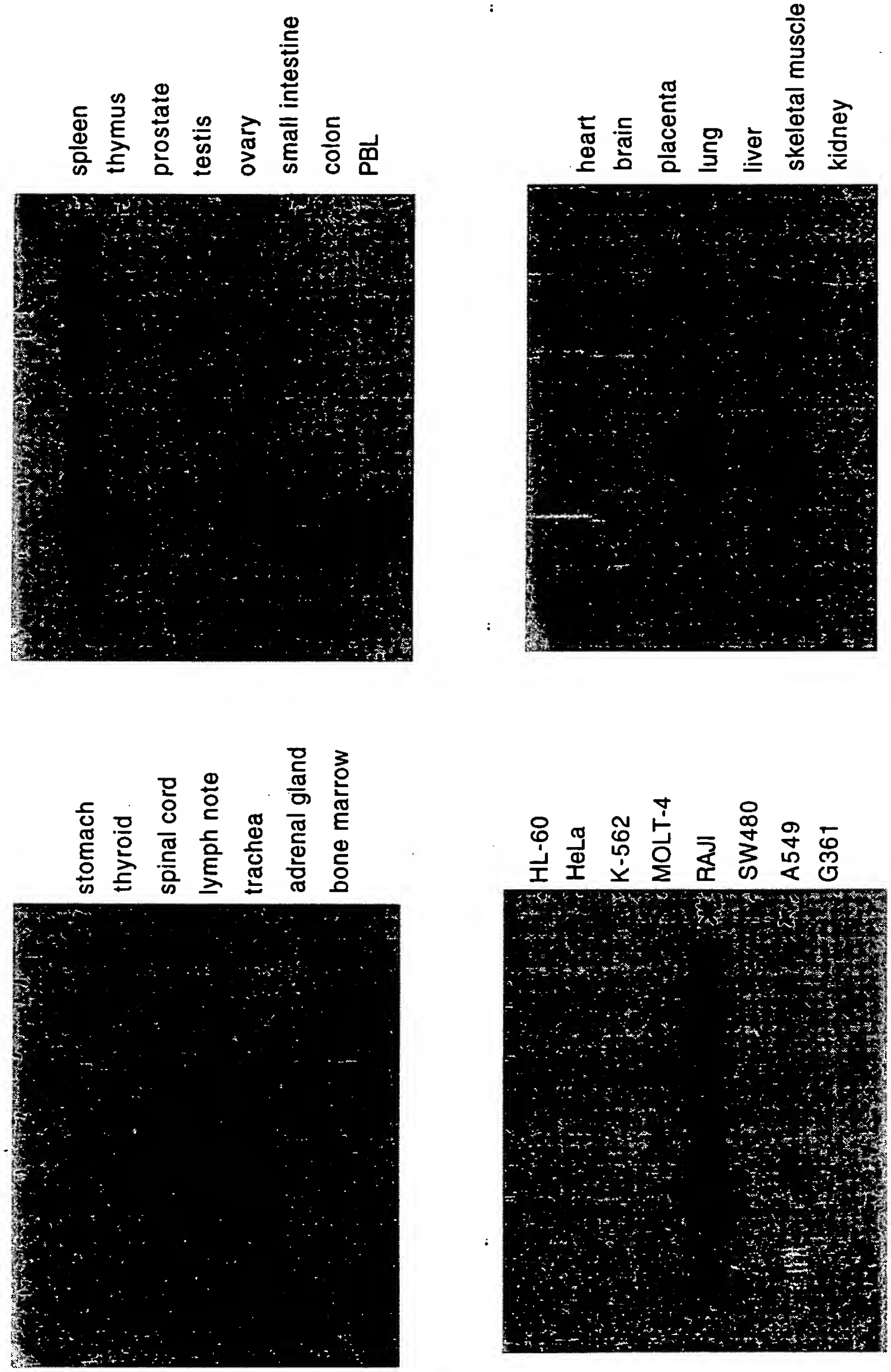
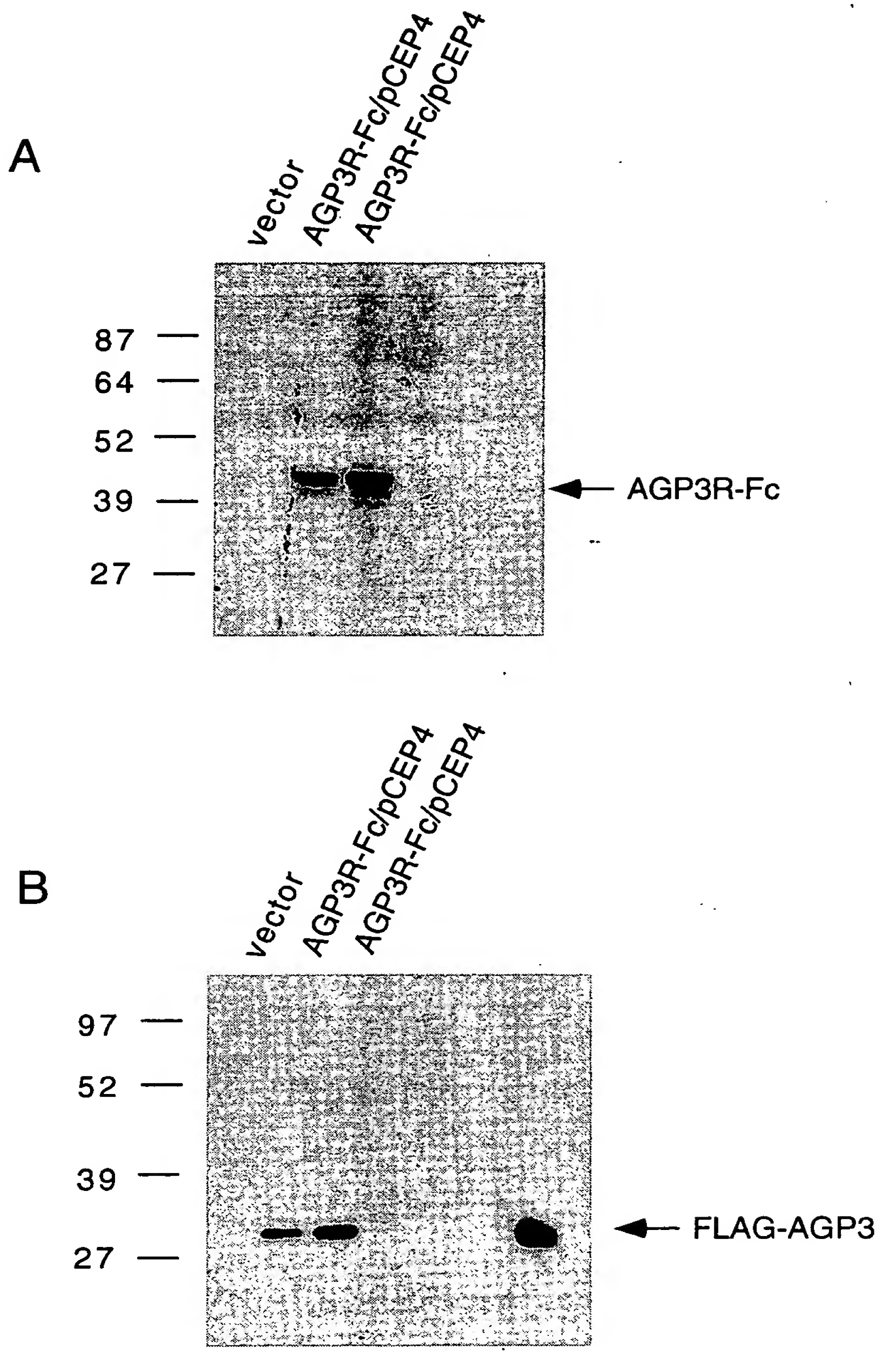


FIG 21


A
vector
AGP3R-Fc/pCEP4
AGP3R-Fc/pCEP4
87
64
52
39
27
AGP3R-Fc
B
vector
AGP3R-Fc/pCEP4
AGP3R-Fc/pCEP4
97
52
39
27
FLAG-AGP3